

*Schwarz*

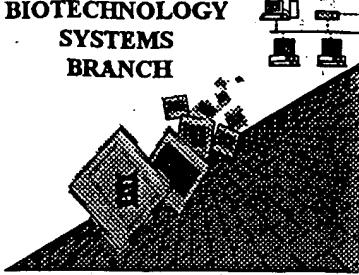
BIOTECHNOLOGY  
SYSTEMS  
BRANCH

# RAW SEQUENCE LISTING

## ERROR REPORT

**BEST AVAILABLE COPY**

*PDX/16*



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/55,514A

Art Unit / Team No.: 1644

Date Processed by STIC: 5/8/2000

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL**

**MARK SPENCER 703-308-4212**

JUN 18 2000  
TC 1600 MAIL ROOM

RECEIVED

R. Schwadron

Page 1 of 24

1644

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514A  
Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

DATE: 05/18/2000  
TIME: 07:15:09

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Kainoh, Mie  
4 Tanaka, Toshiaki  
5 <120> TITLE OF INVENTION: Chimeric proteins, their heterodimer complexes, and platelet substitutes  
6  
7 <130> FILE REFERENCE: 1102-98  
C--> 8  
C--> 9  
9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00370  
10 <151> PRIOR FILING DATE: 1997-01-29  
11 <150> PRIOR APPLICATION NUMBER: JP 9-15118  
12 <151> PRIOR FILING DATE: 1997-01-29  
13 <150> PRIOR APPLICATION NUMBER: JP 9-234544  
14 <151> PRIOR FILING DATE: 1997-08-29  
OK 15 <160> NUMBER OF SEQ ID: 34  
16 <170> SOFTWARE: Microsoft Word 2000

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 4228  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapien  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: 1...2958, 3316...3360, 3480...3808, 3905...4228  
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30 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro  
31 -35 -30 -25  
32 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg 96  
33 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Cys Leu  
34 -20 -15 -10  
35 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg 144  
36 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu  
37 -5 1 5  
38 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg 192  
39 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu  
40 10 15 20 25  
41 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc 240  
42 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala  
43 30 35 40  
44 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga 288  
45 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg  
46 45 50 55  
47 tgc acg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg 336

RAW SEQUENCE LISTING  
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Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

48 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu	
49       60                         65                         70	
50 ggt agc cct aat gga gaa cct tgg tgg aag act tgg ttg gaa gag aga	384
51 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu-Glu Glu Arg	
52       75                         80                         85	
55 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat	432
56 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn	
57       90                         95                         100                         105	
58 gga tcc atc gtg act tgg ggg cat aga tgg aaa aat ata ttt tac ata	480
59 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile	
60       110                         115                         120	
61 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct	528
62 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro	
63       125                         130                         135	
64 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgg tat caa gat	576
65 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp	
66       140                         145                         150	
67 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgg ctt gat gca ata	624
68 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile	
69       155                         160                         165	
70 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca	672
71 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser	
72       170                         175                         180                         185	
73 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa	720
74 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys	
75       190                         195                         200	
76 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat	768
77 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr	
78       205                         210                         215	
79 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc	816
80 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr	
81       220                         225                         230	
82 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat	864
83 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr	
84       235                         240                         245	
85 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa	912
86 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys	
87       250                         255                         260                         265	
88 ggt aaa aag ctt gga tcg tac ttt gga gct tct gtc tgg gct gtc gac	960
89 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp	
90       270                         275                         280	
91 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag	1008
92 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln	
93       285                         290                         295	
94 agc acc atc aga gag gaa gga aga gtt ttt gtg tac atc aac tct ggc	1056
95 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly	
96       300                         305                         310	
97 tcg gga gca gta atg aat gca atg gaa aca aac ctc gtt gga agt gac	1104
98 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp	

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99	315	320	325	
100	aaa tat gct gca aga ttt ggg gaa tct ata gtt aat ctt ggc gac att			1152
101	Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile			
102	330	335	340	345
103	gac aat gat ggc ttt gaa gat gtt gct atc gga gct cca caa gaa gat			1200
104	Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp			
105	350	355	360	
106	gac ttg caa ggt gct att tat att tac aat ggc cgt gca gat ggg atc			1248
107	Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile			
108	365	370	375	
109	tgc tca acc ttc tca cag aga att gaa gga ctt cag atc agc aaa tcg			1296
110	Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser			
111	380	385	390	
112	tta agt atg ttt gga cag tct ata tca gga caa att gat gca gat att			1344
113	Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn			
114	395	400	405	
115	aat ggc tat gta gat gta gca ggt cgt gct ttt cgg tct gat tct gct			1392
116	Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala			
117	410	415	420	425
118	gtc ttg cta agg aca aga cct gta gta att gtt gac gct tct tta agc			1440
119	Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser			
120	430	435	440	
121	cac cct gag tca gta aat aga acg aaa ttt gac tgt gtt gaa aat gga			1488
122	His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly			
123	445	450	455	
124	tgg cct tct gtg tgc ata gat cta aca ctt tgt ttc tca tat aag ggc			1536
125	Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly			
126	460	465	470	
127	aag gaa gtt cca ggt tac att gtt ttg ttt tat aac atg agt ttg gat			1584
128	Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp			
129	475	480	485	
130	gtg aac aag gca gag tct cca cca aga ttc tat ttc tct tct aat			1632
131	Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn			
132	490	495	500	505
133	gga act tct gac gtg att aca gga agc ata cag gtg tcc agc aga gaa			1680
134	Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu			
135	510	515	520	
136	gct aac tgt aga aca cat caa gca ttt atg cgg aaa gat gtg cgg gac			1728
137	Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp			
138	525	530	535	
139	atc ctc acc cca att cag att gaa gct gct tac cac ctt ggt cct cat			1776
140	Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His			
141	540	545	550	
142	gtc atc agt aaa cga agt aca gag gaa ttc cca cca ctt cag cca att			1824
143	Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile			
144	555	560	565	
145	ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt			1872
146	Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe			
147	570	575	580	585

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148	gca	agg	ttt	tgt	gcc	cat	gaa	aat	tgt	tct	gct	gat	tta	cag	gtt	tct		1920
149	Ala	Arg	Phe	Cys	Ala	His	Glu	Asn	Cys	Ser	Ala	Asp	Leu	Gln	Val	Ser		
150					590				595				600					
151	gca	aag	att	ggg	ttt	ttg	aag	ccc	cat	gaa	aat	aaa	aca	tat	ctt	gct		1968
152	Ala	Lys	Ile	Gly	Phe	Leu	Dys	Pro	His	Glu	Asn	Lys	Thr	Tyr	Leu	Ala		
153					605				610			615						
154	gtt	ggg	agt	atg	aag	aca	ttg	atg	ttg	aat	gtg	tcc	ttg	ttt	aat	gct		2016
155	Val	Gly	Ser	Met	Lys	Thr	Leu	Met	Leu	Asn	Val	Ser	Leu	Phe	Asn	Ala		
156					620				625			630						
157	gga	gat	gat	gca	tat	gaa	acg	act	cta	cat	gtc	aaa	cta	ccc	gtg	ggg		2064
158	Gly	Asp	Asp	Ala	Tyr	Glu	Thr	Leu	His	Val	Lys	Leu	Pro	Val	Gly			
159					635				640			645						
160	ctt	tat	ttc	att	aag	att	tta	gag	ctg	gaa	gag	aag	caa	ata	aac	tgt		2112
161	Leu	Tyr	Phe	Ile	Lys	Ile	Leu	Glu	Leu	Glu	Glu	Lys	Gln	Ile	Asn	Cys		
162	650				655				660			665						
163	gaa	gtc	aca	gat	aac	tct	ggc	gtg	gta	caa	ctt	gac	tgc	agt	att	ggc		2160
164	Glu	Val	Thr	Asp	Asn	Ser	Gly	Val	Val	Gln	Leu	Asp	Cys	Ser	Ile	Gly		
165					670				675			680						
166	tat	ata	ata	tat	gta	gat	cat	ctc	tca	agg	ata	gat	att	agc	ttt	ctc	ctg	2208
167	Tyr	Ile	Tyr	Val	Asp	His	Leu	Ser	Arg	Ile	Asp	Ile	Ser	Phe	Leu	Leu		
168					685				690			695						
169	gat	gtg	agc	tca	ctc	agc	aga	gcg	gaa	gag	gac	ctc	agt	atc	aca	gtg		2256
170	Asp	Val	Ser	Ser	Leu	Ser	Arg	Ala	Glu	Glu	Asp	Leu	Ser	Ile	Thr	Val		
171					700				705			710						
172	cat	gct	acc	tgt	gaa	aat	gaa	gag	gaa	atg	gac	aat	cta	aag	cac	agc		2304
173	His	Ala	Thr	Cys	Glu	Asn	Glu	Glu	Met	Asp	Asn	Leu	Lys	His	Ser			
174					715				720			725						
175	aga	gtg	act	gta	gca	ata	cct	tta	aaa	tat	gag	gtt	aag	ctg	act	gtt		2352
176	Arg	Val	Thr	Val	Ala	Ile	Pro	Leu	Lys	Tyr	Glu	Val	Lys	Leu	Thr	Val		
177	730				735				740			745						
178	cat	ggg	ttt	gta	aac	cca	act	tca	ttt	gtg	tat	gga	tca	aat	gat	gaa		2400
179	His	Gly	Phe	Val	Asn	Pro	Thr	Ser	Phe	Val	Tyr	Gly	Ser	Asn	Asp	Glu		
180					750				755			760						
181	aat	gag	cct	gaa	acg	tgc	atg	gtg	gag	aaa	atg	aac	tta	act	ttc	cat		2448
182	Asn	Glu	Pro	Glu	Thr	Cys	Met	Val	Glu	Lys	Met	Asn	Leu	Thr	Phe	His		
183					765				770			775						
184	gtt	atc	aac	act	ggc	aat	agt	atg	gtc	ccc	aat	gtt	agt	gtg	gaa	ata		2496
185	Val	Ile	Asn	Thr	Gly	Asn	Ser	Met	Ala	Pro	Asn	Val	Ser	Val	Glu	Ile		
186					780				785			790						
E-->	187	atg	gtt	cca	aat	tct	ttt	agg	ccc	caa	act	gat	aag	ctg	ttc	aac	att	2588
188	Met	Val	Pro	Asn	Ser	Phe	Ser	Pro	Gln	Thr	Asp	Lys	Leu	Phe	Asn	Ile		2584
189					795				800			805						
190	ttg	gtt	gtc	cag	act	act	act	gga	gaa	tgc	cac	ttt	gaa	aat	tat	caa		2592
191	Leu	Asp	Val	Gln	Thr	Thr	Gly	Glu	Cys	His	Phe	Glu	Asn	Tyr	Gln			
192	810			815				820			825							
193	aga	gtg	tgt	gca	tta	gag	cag	caa	aag	agt	gca	atg	cag	acc	ttg	aaa		2640
194	Arg	Val	Cys	Ala	Leu	Glu	Gln	Gln	Lys	Ser	Ala	Met	Gln	Thr	Leu	Lys		
195					830				835			840						
196	ggc	ata	gtc	cgg	ttc	ttg	tcc	aag	act	gat	aag	agg	cta	ttg	tac	tgc		2688

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Input Set : A:\1102\_98.app  
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197	Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys			
198	845	850	855	
199	ata aaa gct gat cca cat tgt tta aat ttc ttg tgt aat ttt ggg aaa	2736		
200	Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys			
201	860	865	870	
202	atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cggt	2784		
203	Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg			
204	875	880	885	
205	cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata	2832		
206	Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile			
207	890	895	900	905
208	aga gca aca ggt ttt cca gag cca aat cca aga gta att gaa cta aac	2880		
209	Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn			
210	910	915	920	
211	aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa	2928		
212	Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln			
213	925	930	935	
214	aga ccc aaa cgt tat ttc acg gat ccc gag ctgctggaag caggctcagc	2978		
215	Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu			
216	940	945		
217	gctcctgcct ggacgcattcc cggttatgc gccccagttcc agggcagcaa ggcaggcccc	3038		
218	gtctgcctct tcacccggag cctctgcccc cccactcat gtcagggag agggcttct	3098		
219	ggcttttcc caggtctggc gcaggcacag gcttaggtgcc cctaaccacg gcccctgcaca	3158		
220	caaaggggca ggtgtggc tcagacctgc caagagccat atccggggg accctgcccc	3218		
221	tgaccttaagc ccacccaaa ggccaaactc tccactccct cagctcgac accttcttc	3278		
222	ctcccaagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac	3333		
223	Glu Pro Lys Ser Cys Asp			
224	950			
225	aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc	3380		
226	Lys Thr His Thr Cys Pro Pro Cys Pro			
227	955	960		
228	gccctccagc tcaaggcgcc acagggtgcc tagagtagcc tgcatccagg gacaggcccc	3440		
229	agccgggtgc tgacacgtcc acctccatct cttccatca gca cct gaa ctc ctg	3493		
230	Ala Pro Glu Leu Leu			
231	965			
232	ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	3541		
233	Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu			
234	970	975	980	
235	atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gac gtg agc	3589		
236	Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser			
237	985	990	995	
238	cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	3637		
239	His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu			
240	1000	1005	1010	1015
241	gtg cat aat gcc aag aca aag ccg ccg gag gag cag tac aac agc acg	3685		
242	Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr			
243	1020	1025	1030	
244	tac ccg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	3733		
245	Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn			

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246	1035	1040	1045	
247	ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc			3781
248	Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro			
249	1050	1055	1060	
250	atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg			3828
251	Ile Glu Lys Thr Ile Ser Lys Ala Lys			
252	1065	1070		
253	agggccacat ggacagaggc cggtctggcc caccctctgc cctgagagt accgctgtac			3888
255	caacctctgt cctaca ggg cag ccc ega gaa cca cag gtg tac acc ctg			3937
256	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu			
257	1075	1080		
258	ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc			3985
259	Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys			
260	1085	1090	1095	
261	ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc			4033
262	Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser			
263	1100	1105	1110	1115
264	aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gat			4081
265	Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp			
266	1120	1125	1130	
267	tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg gac aag agc			4129
268	Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser			
269	1135	1140	1145	
271	agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct			4177
272	Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala			
273	1150	1155	1160	
274	ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa			4225
275	Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Pro Gly Lys			
276	1165	1170	1175	
277	tga			4228
661	<210> SEQ ID NO: 19			
662	<211> LENGTH: 4675			
663	<212> TYPE: DNA			
664	<213> ORGANISM: Homo sapien			
W->	665 <220> FEATURE:			
666	<221> NAME/KEY: CDS			
667	<222> LOCATION: 1...3405, 3763...3807, 3926...4255, 4352...4675			
W-->	668 <300> PUBLICATION INFORMATION: <i>delete</i>			
W-->	669 <400> SEQUENCE: 19			
670	atg ggg cca gaa cgg aca ggg gcc ggc ccc ctg ctg ctg ctg gtg			48
671	Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val			
672	-25	-20	-15	
673	tta gcg ctc agt caa ggc att tta aat tgt tgt ttg gcc tac aat gtt			96
674	Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val			
675	-10	-5	1	
E-->	676 ggt ctc cca gaa gca aaa ata ttt tcc ggt cct tca agt gaa cag ttt			
677	Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe			
678	5	10	15	
679	ggg tat gca gtg cag cag ttt ata aat cca aaa ggc aac tgg tta ctg			192

(114) 144

TC 1600 MAIL ROOM

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514 A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

680	Gly	Tyr	Ala	Val	Gln	Gln	Phe	Ile	Asn	Pro	Lys	Gly	Asn	Trp	Leu	Leu		
681	20				25				30						35			
682	gtt	ggc	tca	ccc	tgg	agt	ggc	ttt	cct	gag	aac	cga	atg	gga	gat	gtg	240	
683	Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	Glu	Asn	Arg	Met	Gly	Asp	Val		
684															50			
685	tat	aaa	tgt	cct	gtt	gac	cta	tcc	act	gcc	aca	tgt	gaa	aaa	cta	aat	288	
686	Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	Ala	Thr	Cys	Glu	Lys	Leu	Asn		
687															65			
688	ttg	caa	act	tca	aca	aga	cc	aa	t	tt	act	gag	atg	aaa	acc	aac	336	
689	Leu	Gln	Thr	Ser	Thr	Ser	Ile	Pro	Asn	Val	Thr	Glu	Met	Lys	Thr	Asn		
690															80			
691	atg	agc	ctc	ggc	ttg	atc	ctc	acc	agg	aac	atg	gga	act	gga	ggt	ttt	384	
692	Met	Ser	Leu	Gly	Leu	Ile	Leu	Thr	Arg	Asn	Met	Gly	Thr	Gly	Gly	Phe		
693															95			
694	ctc	aca	tgt	gg	cct	ctg	tgg	gca	cag	caa	tgt	ggg	aat	cag	tat	tac	432	
695	Leu	Thr	Cys	Gly	Pro	Leu	Trp	Ala	Gln	Gln	Cys	Gly	Asn	Gln	Tyr	Tyr		
696	100					105				110					115			
697	aca	acg	gg	gt	tgt	tct	gac	atc	agt	cct	gat	ttt	cag	ctc	tca	gcc	480	
698	Thr	Thr	Gly	Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala		
699															130			
700	agc	tcc	tca	cct	gca	act	cag	ccc	tgc	cct	tcc	ctc	ata	gat	gtt	gt	528	
701	Ser	Phe	Ser	Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val		
702						135				140					145			
703	gtt	gt	tgt	gt	aat	gt	att	tat	cct	tgg	gt	gca	gt	aag		576		
704	Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys		
705						150			155						160			
706	aat	ttt	ttg	gaa	aaa	ttt	gta	caa	ggc	ctt	gat	ata	ggc	ccc	aca	aag	624	
707	Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys		
708						165			170						175			
709	aca	cag	gt	gg	tta	att	cag	tat	gcc	aat	aat	cca	aga	gtt	gt	ttt	672	
710	Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe		
711	180					185			190						195			
712	aac	ttt	ttg	aa	ca	aa	acc	aaa	gaa	gaa	atg	att	gt	gca	aca	tcc	720	
713	Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser		
714						200			205						210			
715	cag	aca	tcc	caa	tat	gtt	ggg	gac	ctc	aca	aa	aca	tcc	gga	gca	att	768	
716	Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile		
717						215			220						225			
718	caa	tat	gca	aga	aaa	tat	gcc	tat	tca	gca	gct	tct	gtt	ggg	cga	cga	816	
719	Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg		
720						230			235						240			
721	agt	gt	ac	aa	gt	at	gt	gt	gt	act	gac	gg	gaa	tca	cat	gt	864	
722	Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp	
723						245			250						255			
724	gtt	tca	atg	ttg	aaa	gct	gt	tt	att	gt	caa	tgc	aa	cat	gac	aat	ata	
725	Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile	912	
726	260					265			270						275			
727	ctg	agg	ttt	ggc	ata	gca	gtt	ctt	ggg	tac	tta	aa	cc	aa	gg	cc	tt	960
728	Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu		

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729	280	285	290	
730	gat act aaa aat tta ata aaa gaa ata aaa gcg atc gct agt att cca			1008
731	Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro			
732	295	300	305	
733	aca gaa aga tac ttt ttc aat gtg tct gat gaa gca gct cta cta gaa			1056
734	Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu			
735	310	315	320	
736	aag gct ggg aca tta gga gaa caa att ttc agc att gaa ggt act gtt			1104
737	Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val			
738	325	330	335	
739	caa gga gga gac aac ttt cag atg gaa atg tca caa gtg gga ttc agt			1152
740	Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser			
741	340	345	350	355
742	gca gat tac tct tct aat gat att ctg atg ctg ggt gca gtg gga			1200
743	Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly			
744	360	365	370	
745	gct ttt ggc tgg agt ggg acc att gtc cag aag aca tct cat ggc cat			1248
746	Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His			
747	375	380	385	
748	ttg atc ttt cct aaa caa gcc ttt gac caa att ctg cag gac aga aat			1296
749	Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn			
750	390	395	400	
751	cac agt tca tat tta ggt tac tct gtg gct gca att tct act gga gaa			1344
752	His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu			
753	405	410	415	
754	agc act cac ttt gtt gct ggt gct cct cgg gca aat tat acc ggc cag			1392
755	Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln			
756	420	425	430	435
757	ata gtg cta tat agt gtg aat gag aat ggc aat atc acg gtt att cag			1440
758	Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln			
759	440	445	450	
760	gct cac cga ggt gac cag att ggc tcc tat ttt ggt agt gtg ctg tgt			1488
761	Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys			
762	455	460	465	
763	tca gtt gat gtg gat aaa gac acc att aca gac gtg ctc ttg gta ggt			1536
764	Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Val Gly			
765	470	475	480	
766	gca cca atg tac atg agt gac cta aag aaa gag gaa gga aga gtc tac			1584
767	Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr			
768	485	490	495	
769	ctg ttt act atc aaa aag ggc att ttg ggt cag cac caa ttt ctt gaa			1632
770	Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu			
771	500	505	510	515
772	ggc ccc gag ggc att gaa aac act cga ttt ggt tca gca att gca gct			1680
773	Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala			
774	520	525	530	
775	ctt tca gac atc aac atg gat ggc ttt aat gat gtg att gtt ggt tca			1728
776	Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser			
777	535	540	545	

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778 cca cta gaa aat cag aat tct gga gct gta tac att tac aat ggt cat	1776
779 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His	
780 550 555 560	
781 cag ggc act atc cgc aca aag tat tcc cag aaa atc ttg gga tcc gat	1824
782 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp	
783 565 570 575	
784 gga gcc ttt agg agc cat ctc cag tac ttt ggg agg tcc ttg gat ggc	1872
785 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly	
786 580 585 590 595	
787 tat gga gat tta aat ggg gat tcc atc acc gat gtg tct att ggt gcc	1920
788 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala	
789 600 605 610	
790 ttt gga caa gtg gtt caa ctc tgg tca caa agt att gct gat gta gct	1968
791 Phe Gly Gln Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala	
792 615 620 625	
793 ata gaa gct tca ttc aca cca gaa aaa atc act ttg gtc aac aag aat	2016
794 Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn	
795 630 635 640	
796 gct cag ata att ctc aaa ctc ttc agt gca aag ttc aca cct act	2064
797 Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr	
798 645 650 655	
799 aag caa aac aat caa gtg gcc att gta tat aac atc aca ctt gat gca	2112
800 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala	
801 660 665 670 675	
802 gat gga ttt tca tcc aga gta acc tcc agg ggg tta ttt aaa gaa aac	2160
803 Asp Gly Phe Ser Ser Arg Val Thr Ser Arg Gly Leu Phe Lys Glu Asn	
804 680 685 690	
805 aat gaa agg tgc ctg cag aag aat atg gta gta aat caa gca cag agt	2208
806 Asn Glu Arg Cys Leu Gln Lys Asn Met Val Val Asn Gln Ala Gln Ser	
807 695 700 705	
808 tgc ccc gag cac atc att tat ata cag gag ccc tct gat gtt gtc aac	2256
809 Cys Pro Glu His Ile Ile Tyr Ile Gln Glu Pro Ser Asp Val Val Asn	
810 710 715 720	
811 tct ttg gat ttg cgt gtg gac atc agt ctg gaa aac cct ggc act agc	2304
812 Ser Leu Asp Leu Arg Val Asp Ile Ser Leu Glu Asn Pro Gly Thr Ser	
813 725 730 735	
814 cct gcc ctt gaa gcc tat tct gag act gcc aag gtc ttc agt att cct	2352
815 Pro Ala Leu Glu Ala Tyr Ser Glu Thr Ala Lys Val Phe Ser Ile Pro	
816 740 745 750 755	
817 ttc cac aaa gac tgt ggt gag gat gga ctt tgc att tct gat cta gtc	2400
818 Phe His Lys Asp Cys Gly Glu Asp Gly Leu Cys Ile Ser Asp Leu Val	
819 760 765 770	
820 cta gat gtc cga caa ata cca gct gct caa gaa caa ccc ttt att gtc	2448
821 Leu Asp Val Arg Gln Ile Pro Ala Ala Gln Glu Gln Pro Phe Ile Val	
822 775 780 785	
823 agc aac caa aac aaa agg tta aca ttt tca gta aca ctg aaa aat aaa	2496
824 Ser Asn Gln Asn Lys Arg Leu Thr Phe Ser Val Thr Leu Lys Asn Lys	
825 790 795 800	
826 agg gaa agt gca tac aac act gga att gtt gtt gat ttt tca gaa aac	2544

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Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\1155514.raw

827	Arg	Glu	Ser	Ala	Tyr	Asn	Thr	Gly	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn
828		805						810					815			
829	tgc	ttt	ttt	gca	tca	ttc	tcc	cta	ccg	gtt	gat	ggg	aca	gaa	gta	aca
830	Leu	Phe	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Val	Asp	Gly	Thr	Glu	Val	Thr
831	820							825				830				835
832	tgc	cag	gtg	gct	gca	tct	cag	aag	tct	gtt	gcc	tgc	gat	gta	ggc	tac
833	Cys	Gln	Val	Ala	Ala	Ser	Gln	Lys	Ser	Val	Ala	Cys	Asp	Val	Gly	Tyr
834								840				845				850
835	cct	gct	tta	aag	aga	gaa	caa	cag	gtg	act	ttt	act	att	aac	ttt	gac
836	Pro	Ala	Leu	Lys	Arg	Glu	Gln	Gln	Val	Thr	Phe	Thr	Ile	Asn	Phe	Asp
837								855				860				865
838	ttc	aat	ctt	caa	aac	ctt	cag	aat	cag	gcg	tct	ctc	agt	ttc	caa	gcc
839	Phe	Asn	Leu	Gln	Asn	Leu	Gln	Asn	Gln	Ala	Ser	Leu	Ser	Phe	Gln	Ala
840								870				875				880
841	tta	agt	gaa	agc	caa	gaa	gaa	aac	aag	gct	gat	aat	ttg	gtc	aac	ctc
842	Leu	Ser	Glu	Ser	Gln	Glu	Glu	Asn	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu
843								885				890				895
844	aaa	att	cct	ctc	ctg	tat	gat	gtc	gaa	att	cac	tta	aca	aga	tct	acc
845	Lys	Ile	Pro	Leu	Leu	Tyr	Asp	Ala	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr
846	900							905				910				915
847	aac	ata	aat	ttt	tat	gaa	atc	tct	tcg	gat	ggg	aat	gtt	cct	tca	atc
848	Asn	Ile	Asn	Phe	Tyr	Glu	Ile	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser	Ile
849								920				925				930
850	gtg	cac	agt	ttt	gaa	gat	gtt	ggg	cca	aaa	ttc	atc	ttc	tcc	ctg	aag
851	Val	His	Ser	Phi	Glu	Asp	Val	Gly	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys
852								935				940				945
853	gta	aca	aca	gga	agt	gtt	cca	gta	agc	atg	gca	act	gta	atc	atc	cac
854	Val	Thr	Thr	Gly	Ser	Val	Pro	Val	Ser	Met	Ala	Thr	Val	Ile	Ile	His
855								950				955				960
856	atc	cct	cag	tat	acc	aaa	gaa	aag	aac	cca	ctg	atg	tac	cta	act	ggg
857	Ile	Pro	Gln	Tyr	Thr	Lys	Glu	Lys	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly
858								965				970				975
859	gtg	caa	aca	gac	aag	gct	ggg	gac	atc	agt	tgt	aat	gca	gat	atc	aat
860	Val	Gln	Thr	Asp	Lys	Ala	Gly	Asp	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn
861	980							985				990				995
862	cca	ctg	aaa	ata	gga	caa	aca	tct	tct	tct	gtt	tct	ttc	aaa	agt	gaa
863	Pro	Leu	Lys	Ile	Gly	Gln	Thr	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu	
864								1000				1005				1010
865	aat	ttc	agg	cac	acc	aaa	gaa	ttg	aac	tgc	aga	act	gct	tcc	tgt	agt
866	Asn	Phe	Arg	His	Thr	Lys	Glu	Leu	Asn	Cys	Arg	Thr	Ala	Ser	Cys	Ser
867								1015				1020				1025
868	aat	gtt	acc	tgc	tgg	ttg	aaa	gac	gtt	cac	atg	aaa	gga	gaa	tac	ttt
869	Asn	Val	Thr	Cys	Trp	Leu	Lys	Asp	Val	His	Met	Lys	Gly	Thy	Tyr	Phe
870								1030				1035				1040
871	gtt	aat	gtg	act	acc	aga	att	tgg	aac	ggg	act	ttc	gca	tca	tca	acg
872	Val	Asn	Val	Thr	Thr	Arg	Ile	Trp	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr
873								1045				1050				1055
874	ttc	cag	aca	gta	cag	cta	acg	gca	gct	gca	gaa	atc	aac	acc	tat	aac
875	Phe	Gln	Thr	Val	Gln	Leu	Thr	Ala	Ala	Ala	Glu	Ile	Asn	Thr	Tyr	Asn

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876	1060	1065	1070	1075
877	cct gag ata tat gtg att gaa gat aac act gtt acg att ccc ctg atg			3360
878	Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met			
879	1080	1085	1090	
880	ata atg aaa cct gat gag aaa gcc gaa gta cca aca gat ccc gag			3405
881	Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu			
882	1095	1100	1105	
883	ctgttggaaag caggctcgcg gtcctgtcgt ggacgcattcc cggctatcgcc gccccatgtcc	3465		
884	aggccagcaa ggccggcccc gtcgtcccttc tcaaccggag cctctggcccccactcat	3525		
885	gctcaggagg aggttcttcc ggcttttcc caggctctgg gcaggcacag gctagggtgcc	3585		
886	cctaaccagg gcctgcaca caaaggggca ggtgtggc tcagaccgtc caagaggccat	3645		
887	atccgggg accctgtccccc tgacctaagc ccacccaaactt ggcacaaatcc tccactccct	3705		
888	cagctggac accttctctc ctcccgaggat ccagaacttcc ccaatcttct ctctgc	3762		
889	gac ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca	3807		
890	Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro			
891	1110	1115	1120	
892	ggtaaaggccg cccaggccctc gcctccgc tcaaggccggg acaggtgccc tagtagtgcc	3867		
893	tgcattccagg gagccggcccc agccgggtgc tgacacgtcc accttcattcttccctca	3925		
894	gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa	3973		
895	Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys			
896	1125	1130	1135	
897	ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg	4021		
898	Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val			
899	1140	1145	1150	
900	gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac	4069		
901	Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr			
902	1155	1160	1165	
904	gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg ccg gag gag	4117		
905	Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu			
906	1170	1175	1180	1185
907	cag tac aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac	4165		
908	Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His			
909	1190	1195	1200	
910	cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa	4213		
911	Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys			
912	1205	1210	1215	
913	gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa	4255		
914	Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys			
915	1220	1225	1230	
916	gggtggggaccc gtgggggtcg aggccacat ggacagaggcc cggtctggcc cacccttcgtc	4315		
917	cctgagatgt accgtgtac caaacctgtt cctaca ggg cag ccc cga gaa cca	4369		
918	Gly Gln Pro Arg Glu Pro			
919	1235			
920	cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag	4417		
921	Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln			
922	1240	1245	1250	
923	gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc	4465		
924	Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
925	1255	1260	1265	

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926	gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg	4513
927	Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr	
928	1270 1275 1280 1285	
929	cct ccc gtg ctg gat tcc gac ggc tcc ttc ctc tac agc aag ctc	4561
930	Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu	
931	1290 1295 1300	
932	acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc	4609
933	Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser	
934	1305 1310 1315	
935	gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc	4657
936	Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser	
937	1320 1325 1330	
938	ctg tct ccg ggt aaa tga	4675
939	Leu Ser Pro Gly Lys	
940	1335	
1077	<210> SEQ ID NO: 32	
1078	<211> LENGTH: 1179	
1079	<212> TYPE: PRT	
1080	<213> ORGANISM: Homo sapien	
1082	<400> SEQUENCE: 32	
1083	Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Arg Gly Ala Asn Pro	
1084	-35 -30 -25	
1086	Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Cys Leu	
1087	-20 -15 -10	
1089	Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu	
1090	-5 1 5	
1092	Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu	
1093	10 15 20 25	
1095	His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala	
1096	30 35 40	
1098	Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg	
1099	45 50 55	
1101	Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu	
1102	60 65 70	
1104	Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg	
1105	75 80 85	
1107	Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn	
1108	90 95 100 105	
1110	Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile	
1111	110 115 120	
1113	Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro	
1114	125 130 135	
1116	Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp	
1117	140 145 150	
1119	Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile	
1120	155 160 165	
1122	Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser	
1123	170 175 180 185	
1125	Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys	

(1218 (p. 15) (please include negative numbers in  
 (2117 response))

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

1126	190	195	200
1128	Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr		
1129	205	210	215
1131	Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr		
1132	220	225	230
1135	Glu Val Val Gly Gly Ala Pro Gin His Glu Gln Ile Gly Lys Ala Tyr		
1136	235	240	245
1138	Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys		
1139	250	255	260
1141	Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp		
1142	270	275	280
1144	Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln		
1145	285	290	295
1147	Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly		
1148	300	305	310
1150	Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp		
1151	315	320	325
1153	Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile		
1154	330	335	340
1156	Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp		
1157	350	355	360
1159	Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile		
1160	365	370	375
1162	Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser		
1163	380	385	390
1165	Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn		
1166	395	400	405
1168	Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala		
1169	410	415	420
1171	Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser		
1172	430	435	440
1174	His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly		
1175	445	450	455
1177	Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly		
1178	460	465	470
1180	Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp		
1181	475	480	485
1183	Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn		
1184	490	495	500
1186	Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu		
1187	510	515	520
1189	Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp		
1190	525	530	535
1192	Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His		
1193	540	545	550
1195	Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile		
1196	555	560	565
1198	Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe		
1199	570	575	580

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

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1201 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser
1202      590      595      600
1204 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala
1205      605      610      615
1207 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala
1208      620      625      630
1210 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly
1211      635      640      645
1213 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Lys Gln Ile Asn Cys
1214 650      655      660      665
1216 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly
1217      670      675      680
1219 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu
1220      685      690      695
1222 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val
1223      700      705      710
1225 His Ala Thr Cys Glu Asn Glu Glu Met Asp Asn Leu Lys His Ser
1226      715      720      725
1228 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val
1229 730      735      740      745
1231 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu
1232      750      755      760
1234 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His
1235      765      770      775
1237 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile
1238      780      785      790
1240 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile
1241      795      800      805
1243 Leu Asp Val Gln Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
1244 810      815      820      825
1246 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
1247      830      835      840
1249 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
1250      845      850      855
1252 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
1253      860      865      870
1255 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
1256      875      880      885
1258 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
1259 890      895      900      905
1261 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
1262      910      915      920
1264 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
1265      925      930      935
1267 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu Glu Pro Lys Ser Cys Asp
1268      940      945      950
1270 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
1271      955      960      965
1273 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

1274	970	975	980	985
1276	Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu			
1277	990	995	1000	
1279	Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His			
1280	1005	1010	1015	
1282	Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg			
1283	1020	1025	1030	
1285	Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys			
1286	1035	1040	1045	
1288	Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu			
1289	1050	1055	1060	1065
1291	Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr			
1292	1070	1075	1080	
1294	Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu			
1295	1085	1090	1095	
1297	Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp			
1298	1100	1105	1110	
1300	Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val			
1301	1115	1120	1125	
1303	Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp			
1304	1130	1135	1140	1145
1306	Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His			
1307	1150	1155	1160	
1309	Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro			
1310	1165	1170	1175	

E--> 1312 Gly Lys

1315	<210> SEQ ID NO: 33			
1316	<211> LENGTH: 943	963	(p. 18)	
1317	<212> TYPE: PRT			
1318	<213> ORGANISM: Homo sapien			
1320	<400> SEQUENCE: 33			
1323	Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile Ser Ser Val Cys			
1324	-20	-15	-10	-5
1326	Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala			
1327	1	5	10	
1329	Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys			
1330	15	20	25	
1332	Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys			
1333	30	35	40	
1335	Asp Asp Leu Glu Ala Leu Lys Lys Gly Cys Pro Pro Asp Asp Ile			
1336	45	50	55	60
1338	Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr			
1339	65	70	75	
1341	Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His			
1342	80	85	90	
1344	Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro			
1345	95	100	105	
1347	Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp			
1348	110	115	120	

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

1351 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu  
 1352 125 130 135 140  
 1354 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile  
 1355 145 150 155  
 1357 Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val  
 1358 160 165 170  
 1360 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr  
 1361 175 180 185  
 1363 Ser Glu Gln Asn Cys Thr Thr Pro Phe Ser Tyr Lys Asn Val Leu Ser  
 1364 190 195 200  
 1366 Leu Thr Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys Gln Arg  
 1367 205 210 215 220  
 1369 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met  
 1370 225 230 235  
 1372 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg  
 1373 240 245 250  
 1375 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly  
 1376 255 260 265  
 1378 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu  
 1379 270 275 280  
 1381 Asn Asn Met Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala  
 1382 285 290 295 300  
 1384 His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala  
 1385 305 310 315  
 1387 Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile  
 1388 320 325 330  
 1390 Pro Lys Ser Ala Val Gly Thr Leu Ser Ala Asn Ser Ser Asn Val Ile  
 1391 335 340 345  
 1393 Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu  
 1394 350 355 360  
 1396 Glu Asn Gly Lys Leu Ser Glu Gly Val Thr Ile Ser Tyr Lys Ser Tyr  
 1397 365 370 375 380  
 1399 Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser  
 1400 385 390 395  
 1402 Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ser  
 1403 400 405 410  
 1405 Asn Lys Cys Pro Lys Lys Asp Ser Asp Ser Phe Lys Ile Arg Pro Leu  
 1406 415 420 425  
 1408 Gly Phe Thr Glu Glu Val Glu Val Ile Leu Gln Tyr Ile Cys Glu Cys  
 1409 430 435 440  
 1411 Glu Cys Gln Ser Glu Gly Ile Pro Glu Ser Pro Lys Cys His Glu Gly  
 1412 445 450 455 460  
 1414 Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val  
 1415 465 470 475  
 1417 Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met  
 1418 480 485 490  
 1420 Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn  
 1421 495 500 505  
 1423 Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
 TIME: 07:15:09

Input Set : A:\1102\_98.app  
 Output Set: N:\CRF3\05182000\I155514.raw

1424	510	515	520
1426	Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys		
1427	525	530	535
1429	Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys		540
1430	545	550	555
1432	Arg Val Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys		
1433	560	565	570
1435	Ser Leu Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn		
1436	575	580	585
1438	Gly Arg Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp Pro Lys		
1439	590	595	600
1441	Phe Gln Gly Gln Thr Cys Glu Met Cys Gln Thr Cys Leu Gly Val Cys		
1442	605	610	615
1444	Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu		620
1445	625	630	635
1447	Lys Lys Asp Thr Cys Thr Gln Glu Cys Ser Tyr Phe Asn Ile Thr Lys		
1448	640	645	650
1450	Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val		
1451	655	660	665
1453	Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr		
1454	670	675	680
1456	Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn		
1457	685	690	695
1459	Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu Glu Pro Lys Ser Cys		700
1460	705	710	715
1462	Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
1463	720	725	730
1465	Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
1466	735	740	745
1468	Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
1469	750	755	760
1471	Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
1472	765	770	775
1474	His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		780
1475	785	790	795
1477	Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
1478	800	805	810
1480	Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		
1481	815	820	825
1483	Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
1484	830	835	840
1486	Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		
1487	845	850	855
1489	Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		860
1490	865	870	875
1492	Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
1493	880	885	890
1495	Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val		
1496	895	900	905

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514A

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TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

1498 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
1499 910 915 920  
1501 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
1502 925 930 935 940

E--> 1504 Pro Gly Lys

1506 <210> SEQ ID NO: 34  
<211> LENGTH: 1338

1508 <212> TYPE: PRT

1509 <213> ORGANISM: Homo sapien

W--> 1510 <300> PUBLICATION INFORMATION:

1512 <400> SEQUENCE: 34

1513 Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Val  
1514 -25 -20 -15  
1516 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val  
1517 -10 -5 1  
1519 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe  
1520 5 10 15  
1522 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu  
1523 20 25 30 35  
1525 Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val  
1526 40 45 50  
1528 Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn  
1529 55 60 65  
1531 Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn  
1532 70 75 80  
1534 Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Phe  
1535 85 90 95  
1537 Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr  
1538 100 105 110 115  
1540 Thr Thr Gly Val Cys Ser Asp Ile Ser Pro Asp Phe Gln Leu Ser Ala  
1541 120 125 130  
1543 Ser Phe Ser Pro Ala Thr Gln Pro Cys Pro Ser Leu Ile Asp Val Val  
1544 135 140 145  
1546 Val Val Cys Asp Glu Ser Asn Ser Ile Tyr Pro Trp Asp Ala Val Lys  
1547 150 155 160  
1549 Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys  
1550 165 170 175  
1552 Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Val Val Phe  
1553 180 185 190 195  
1555 Asn Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser  
1556 200 205 210  
1558 Gln Thr Ser Gln Tyr Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile  
1559 215 220 225  
1561 Gln Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg  
1562 230 235 240  
1564 Ser Ala Thr Lys Val Met Val Val Thr Asp Gly Glu Ser His Asp  
1565 245 250 255  
1567 Gly Ser Met Leu Lys Ala Val Ile Asp Gln Cys Asn His Asp Asn Ile  
1568 260 265 270 275

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514 A

DATE: 05/18/2000  
TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

1570 Leu Arg Phe Gly Ile Ala Val Leu Gly Tyr Leu Asn Arg Asn Ala Leu  
1571 280 285 290  
1573 Asp Thr Lys Asn Leu Ile Lys Glu Ile Lys Ala Ile Ala Ser Ile Pro  
1574 295 300 305  
1576 Thr Glu Arg Tyr Phe Phe Asn Val Ser Asp Glu Ala Ala Leu Leu Glu  
1577 310 315 320  
1579 Lys Ala Gly Thr Leu Gly Glu Gln Ile Phe Ser Ile Glu Gly Thr Val  
1580 325 330 335  
1582 Gln Gly Gly Asp Asn Phe Gln Met Glu Met Ser Gln Val Gly Phe Ser  
1583 340 345 350 355  
1585 Ala Asp Tyr Ser Ser Gln Asn Asp Ile Leu Met Leu Gly Ala Val Gly  
1586 360 365 370  
1588 Ala Phe Gly Trp Ser Gly Thr Ile Val Gln Lys Thr Ser His Gly His  
1589 375 380 385  
1591 Leu Ile Phe Pro Lys Gln Ala Phe Asp Gln Ile Leu Gln Asp Arg Asn  
1592 390 395 400  
1594 His Ser Ser Tyr Leu Gly Tyr Ser Val Ala Ala Ile Ser Thr Gly Glu  
1595 405 410 415  
1597 Ser Thr His Phe Val Ala Gly Ala Pro Arg Ala Asn Tyr Thr Gly Gln  
1598 420 425 430 435  
1600 Ile Val Leu Tyr Ser Val Asn Glu Asn Gly Asn Ile Thr Val Ile Gln  
1601 440 445 450  
1603 Ala His Arg Gly Asp Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Cys  
1604 455 460 465  
1606 Ser Val Asp Val Asp Lys Asp Thr Ile Thr Asp Val Leu Leu Val Gly  
1607 470 475 480  
1609 Ala Pro Met Tyr Met Ser Asp Leu Lys Lys Glu Glu Gly Arg Val Tyr  
1610 485 490 495  
1612 Leu Phe Thr Ile Lys Lys Gly Ile Leu Gly Gln His Gln Phe Leu Glu  
1613 500 505 510 515  
1615 Gly Pro Glu Gly Ile Glu Asn Thr Arg Phe Gly Ser Ala Ile Ala Ala  
1616 520 525 530  
1618 Leu Ser Asp Ile Asn Met Asp Gly Phe Asn Asp Val Ile Val Gly Ser  
1619 535 540 545  
1621 Pro Leu Glu Asn Gln Asn Ser Gly Ala Val Tyr Ile Tyr Asn Gly His  
1622 550 555 560  
1624 Gln Gly Thr Ile Arg Thr Lys Tyr Ser Gln Lys Ile Leu Gly Ser Asp  
1625 565 570 575  
1627 Gly Ala Phe Arg Ser His Leu Gln Tyr Phe Gly Arg Ser Leu Asp Gly  
1628 580 585 590 595  
1630 Tyr Gly Asp Leu Asn Gly Asp Ser Ile Thr Asp Val Ser Ile Gly Ala  
1631 600 605 610  
1633 Phe Gly Gln Val Val Gln Leu Trp Ser Gln Ser Ile Ala Asp Val Ala  
1634 615 620 625  
1636 Ile Glu Ala Ser Phe Thr Pro Glu Lys Ile Thr Leu Val Asn Lys Asn  
1637 630 635 640  
1639 Ala Gln Ile Ile Leu Lys Leu Cys Phe Ser Ala Lys Phe Arg Pro Thr  
1640 645 650 655  
1642 Lys Gln Asn Asn Gln Val Ala Ile Val Tyr Asn Ile Thr Leu Asp Ala

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514A

DATE: 05/18/2000  
TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

1643	660	665	670	675													
1645	Asp	Gly	Phe	Ser	Ser	Arg	Val	Thr	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn	
1646																	
1648																	
1649																	
1651	Cys	Pro	Glu	His	Ile	Ile	Tyr	Ile	Gln	Glu	Pro	Ser	Asp	Val	Val	Asn	
1652																	
1654	Ser	Leu	Asp	Leu	Arg	Val	Asp	Ile	Ser	Leu	Glu	Asn	Pro	Gly	Thr	Ser	
1655																	
1657	Pro	Ala	Leu	Glu	Ala	Tyr	Ser	Glu	Thr	Ala	Lys	Val	Phe	Ser	Ile	Pro	
1658																	
1660	Phe	His	Lys	Asp	Cys	Gly	Glu	Asp	Gly	Leu	Cys	Ile	Ser	Asp	Leu	Val	
1661																	
1663	Leu	Asp	Val	Arg	Gln	Ile	Pro	Ala	Ala	Gln	Glu	Gln	Pro	Phe	Ile	Val	
1664																	
1666	Ser	Asn	Gln	Asn	Lys	Arg	Leu	Thr	Phe	Ser	Val	Thr	Leu	Lys	Asn	Lys	
1667																	
1669	Arg	Glu	Ser	Ala	Tyr	Asn	Thr	Gly	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn	
1670																	
1672	Leu	Phe	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Val	Asp	Gly	Thr	Glu	Val	Thr	
1673																	
1675	Cys	Gln	Val	Ala	Ala	Ser	Gln	Lys	Ser	Val	Ala	Cys	Asp	Val	Gly	Tyr	
1676																	
1678	Pro	Ala	Leu	Lys	Arg	Glu	Gln	Gln	Val	Thr	Phe	Thr	Ile	Asn	Phe	Asp	
1679																	
1681	Phe	Asn	Leu	Gln	Asn	Leu	Gln	Asn	Gln	Ala	Ser	Leu	Ser	Phe	Gln	Ala	
1682																	
1684	Leu	Ser	Glu	Ser	Gln	Glu	Glu	Asn	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu	
1685																	
1687	Lys	Ile	Pro	Leu	Leu	Tyr	Asp	Ala	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr	
1688																	
1690	Asn	Ile	Asn	Phe	Tyr	Glu	Ile	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser	Ile	
1691																	
1693	Val	His	Ser	Phe	Glu	Asp	Val	Gly	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys	
1694																	
1696	Val	Thr	Thr	Gly	Ser	Val	Pro	Val	Ser	Met	Ala	Thr	Val	Ile	Ile	His	
1697																	
1699	Ile	Pro	Gln	Tyr	Thr	Lys	Glu	Lys	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly	
1700																	
1702	Val	Gln	Thr	Asp	Lys	Ala	Gly	Asp	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn	
1703																	
1705	Pro	Leu	Lys	Ile	Gly	Gln	Thr	Ser	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu	
1706																	
1708	Asn	Phe	Arg	His	Thr	Lys	Glu	Leu	Asn	Cys	Arg	Thr	Ala	Ser	Cys	Ser	
1709																	
1711	Asn	Val	Thr	Cys	Trp	Leu	Lys	Asp	Val	His	Met	Lys	Gly	Glu	Tyr	Phe	
1712																	
1714	Val	Asn	Val	Thr	Thr	Arg	Ile	Trp	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr	
1715																	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/155,514 A

DATE: 05/18/2000  
TIME: 07:15:09

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

```

1717 Phe Gln Thr Val Gln Leu Thr Ala Ala Glu Ile Asn Thr Tyr Asn
1718 1060          1065          1070          1075
1720 Pro Glu Ile Tyr Val Ile Glu Asp Asn Thr Val Thr Ile Pro Leu Met
1721          1080          1085          1090
1723 Ile Met Lys Pro Asp Glu Lys Ala Glu Val Pro Thr Asp Pro Glu Glu
1724          1095          1100          1105
1726 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
1727          1110          1115          1120
1729 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
1730          1125          1130          1135
1732 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
1733 1140          1145          1150          1155
1735 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
1736          1160          1165          1170
1738 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Gin Tyr
1739          1175          1180          1185
1741 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
1742          1190          1195          1200
1744 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
1745 1205          1210          1215
1747 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
1748 1220          1225          1230          1235
1750 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
1751          1240          1245          1250
1753 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
1754          1255          1260          1265
1756 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
1757          1270          1275          1280
1759 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
1760 1285          1290          1295
1762 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
1763 1300          1305          1310          1315
1765 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
1766          1320          1325          1330
1768 Leu Ser Leu Ser Pro Gly Lys
E--> 1769          1335

```

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/155,514A DATE: 05/18/2000  
TIME: 07:15:10

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:7 M:283 W: Missing Blank Line separator, <130> field identifier  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:283 W: Missing Blank Line separator, <160> field identifier  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:25 M:283 W: Missing Blank Line separator, <300> field identifier  
L:187 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:2588 Counted:2544  
L:284 M:283 W: Missing Blank Line separator, <220> field identifier  
L:287 M:283 W: Missing Blank Line separator, <300> field identifier  
L:288 M:283 W: Missing Blank Line separator, <400> field identifier  
L:496 M:283 W: Missing Blank Line separator, <220> field identifier  
L:496 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:508 M:283 W: Missing Blank Line separator, <220> field identifier  
L:509 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:511 M:283 W: Missing Blank Line separator, <400> field identifier  
L:518 M:283 W: Missing Blank Line separator, <220> field identifier  
L:519 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:521 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:283 W: Missing Blank Line separator, <220> field identifier  
L:529 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:531 M:283 W: Missing Blank Line separator, <400> field identifier  
L:539 M:283 W: Missing Blank Line separator, <220> field identifier  
L:540 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:552 M:283 W: Missing Blank Line separator, <220> field identifier  
L:553 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:555 M:283 W: Missing Blank Line separator, <400> field identifier  
L:562 M:283 W: Missing Blank Line separator, <220> field identifier  
L:563 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:565 M:283 W: Missing Blank Line separator, <400> field identifier  
L:572 M:283 W: Missing Blank Line separator, <220> field identifier  
L:573 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:575 M:283 W: Missing Blank Line separator, <400> field identifier  
L:582 M:283 W: Missing Blank Line separator, <220> field identifier  
L:583 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:585 M:283 W: Missing Blank Line separator, <400> field identifier  
L:592 M:283 W: Missing Blank Line separator, <220> field identifier  
L:593 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:595 M:283 W: Missing Blank Line separator, <400> field identifier  
L:602 M:283 W: Missing Blank Line separator, <220> field identifier  
L:603 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:605 M:283 W: Missing Blank Line separator, <400> field identifier  
L:612 M:283 W: Missing Blank Line separator, <220> field identifier  
L:613 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:615 M:283 W: Missing Blank Line separator, <400> field identifier  
L:622 M:283 W: Missing Blank Line separator, <220> field identifier  
L:623 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:625 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/155,514 A

DATE: 05/18/2000  
TIME: 07:15:10

Input Set : A:\1102\_98.app  
Output Set: N:\CRF3\05182000\I155514.raw

L:632 M:283 W: Missing Blank Line separator, <220> field identifier  
L:632 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:635 M:283 W: Missing Blank Line separator, <400> field identifier  
L:643 M:283 W: Missing Blank Line separator, <220> field identifier  
L:643 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:646 M:283 W: Missing Blank Line separator, <400> field identifier  
L:654 M:283 W: Missing Blank Line separator, <220> field identifier  
L:654 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:657 M:283 W: Missing Blank Line separator, <400> field identifier  
L:665 M:283 W: Missing Blank Line separator, <220> field identifier  
L:668 M:283 W: Missing Blank Line separator, <300> field identifier  
L:669 M:283 W: Missing Blank Line separator, <400> field identifier  
L:676 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:114 Counted:144  
L:946 M:283 W: Missing Blank Line separator, <220> field identifier  
L:947 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:949 M:283 W: Missing Blank Line separator, <400> field identifier  
L:956 M:283 W: Missing Blank Line separator, <220> field identifier  
L:957 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21  
L:959 M:283 W: Missing Blank Line separator, <400> field identifier  
L:967 M:283 W: Missing Blank Line separator, <220> field identifier  
L:968 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22  
L:970 M:283 W: Missing Blank Line separator, <400> field identifier  
L:977 M:283 W: Missing Blank Line separator, <220> field identifier  
L:978 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
L:980 M:283 W: Missing Blank Line separator, <400> field identifier  
L:987 M:283 W: Missing Blank Line separator, <220> field identifier  
L:987 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:999 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1010 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1021 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1032 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1043 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1054 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1066 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:1312 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:1179 Counted:1218  
L:1504 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:943 Counted:963  
L:1769 M:252 E: (20) Calc# of Seq. differs from actual, <211> LENGTH:Input:1338 Counted:1367